## **RAW SEQUENCE LISTING**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

09/150,947 G
TEW16
09/15/2005

# ENTERED



IFW16

RAW SEQUENCE LISTING DATE: 09/15/2005
PATENT APPLICATION: US/09/150,947G TIME: 11:40:46

Input Set : A:\sequence listing.txt

Output Set: N:\CRF4\09152005\I150947G.raw

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3 <110> APPLICANT: KAEMPFER, Raymond
        ARAD, Gila
 6 <120> TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS ANTAGONISTS VACCINES
 8 <130> FILE REFERENCE: KAEMPFER1
10 <140> CURRENT APPLICATION NUMBER: 09/150,947G
11 <141> CURRENT FILING DATE: 1998-09-10
13 <150> PRIOR APPLICATION NUMBER: PCT/IL97/00438
14 <151> PRIOR FILING DATE: 1997-12-30
16 <150> PRIOR APPLICATION NUMBER: ISRAEL 119938
17 <151> PRIOR FILING DATE: 1996-12-30
19 <160> NUMBER OF SEQ ID NOS: 15
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 12
25 <212> TYPE: PRT
26 <213> ORGANISM: Staphylococcus aureus
28 <400> SEQUENCE: 1
30 Thr Asn Lys Lys Val Thr Ala Gln Glu Leu Asp
34 <210> SEQ ID NO: 2
35 <211> LENGTH: 12
36 <212> TYPE: PRT
37 <213> ORGANISM: Staphylococcus aureus
39 <400> SEQUENCE: 2
41 Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp
45 <210> SEO ID NO: 3
46 <211> LENGTH: 10
47 <212> TYPE: PRT
48 <213> ORGANISM: Staphylococcus aureus
50 <400> SEQUENCE: 3
52 Lys Lys Val Thr Ala Gln Glu Leu Asp
53 1
56 <210> SEQ ID NO: 4
57 <211> LENGTH: 10
58 <212> TYPE: PRT
59 <213> ORGANISM: Staphylococcus aureus
61 <400> SEQUENCE: 4
63 Lys Lys Lys Ala Thr Val Gln Glu Leu Asp
64 1
                   5
67 <210> SEQ ID NO: 5
68 <211> LENGTH: 13
69 <212> TYPE: PRT
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Input Set : A:\sequence listing.txt
Output Set: N:\CRF4\09152005\I150947G.raw

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70 <213> ORGANISM: Staphylococcus aureus
73 <220> FEATURE:
74 <221> NAME/KEY: LIPID
75 <222> LOCATION: (1)..(1)
76 <223> OTHER INFORMATION: N-lauryl cysteine residue
78 <400> SEQUENCE: 5
80 Cys Thr Asn Lys Lys Lys Val Thr Ala Gln Glu Leu Asp
84 <210> SEQ ID NO: 6
85 <211> LENGTH: 13
86 <212> TYPE: PRT
87 <213> ORGANISM: Staphylococcus aureus
90 <220> FEATURE:
91 <221> NAME/KEY: LIPID
92 <222> LOCATION: (1)..(1)
93 <223> OTHER INFORMATION: N-lauryl cysteine residue
95 <400> SEQUENCE: 6
97 Cys Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp
98 1
101 <210> SEQ ID NO: 7
102 <211> LENGTH: 24
103 <212> TYPE: PRT
104 <213> ORGANISM: Staphylococcus aureus
106 <400> SEQUENCE: 7
108 Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp Tyr Asn Lys Lys
109 1
112 Lys Ala Thr Val Gln Glu Leu Asp
113
                20
116 <210> SEQ ID NO: 8
117 <211> LENGTH: 36
118 <212> TYPE: PRT
119 <213> ORGANISM: Staphylococcus aureus
121 <400> SEQUENCE: 8
123 Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp Tyr Asn Lys Lys
                                         10
127 Lys Ala Thr Val Gln Glu Leu Asp Tyr Asn Lys Lys Ala Thr Val
128
                20
                                    25
131 Gln Glu Leu Asp
132
            35
135 <210> SEQ ID NO: 9
136 <211> LENGTH: 14
137 <212> TYPE: PRT
138 <213> ORGANISM: Staphylococcus aureus
141 <220> FEATURE:
142 <221> NAME/KEY: DISULFID
143 <222> LOCATION: (1)..(1)
145 <220> FEATURE:
146 <221> NAME/KEY: DISULFID
147 <222> LOCATION: (14)..(14)
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Input Set : A:\sequence listing.txt
Output Set: N:\CRF4\09152005\I150947G.raw

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149 <400> SEOUENCE: 9
151 Cys Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp Cys
152 1
155 <210> SEQ ID NO: 10
156 <211> LENGTH: 14
157 <212> TYPE: PRT
158 <213> ORGANISM: Staphylococcus aureus
161 <220> FEATURE:
162 <221> NAME/KEY: MOD_RES
163 <222> LOCATION: (1)..(1)
164 <223> OTHER INFORMATION: D-alanine
166 <220> FEATURE:
167 <221> NAME/KEY: MOD RES
168 <222> LOCATION: (14)..(14)
169 <223> OTHER INFORMATION: D-alanine
171 <400> SEQUENCE: 10
173 Ala Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp Ala
174 1
177 <210> SEQ ID NO: 11
178 <211> LENGTH: 13
179 <212> TYPE: PRT
180 <213> ORGANISM: Staphylococcus aureus
183 <220> FEATURE:
184 <221> NAME/KEY: ACETYLATION
185 <222> LOCATION: (1)..(1)
187 <220> FEATURE:
188 <221> NAME/KEY: MOD RES
189 <222> LOCATION: (13)..(13)
190 <223> OTHER INFORMATION: D-alanine
192 <400> SEQUENCE: 11
194 Tyr Asn Lys Lys Lys Ala Thr Val Gln Glu Leu Asp Ala
195 1
                    5
198 <210> SEQ ID NO: 12
199 <211> LENGTH: 239
200 <212> TYPE: PRT
201 <213> ORGANISM: Staphylococcus aureus
203 <400> SEQUENCE: 12
205 Glu Ser Gln Pro Asp Pro Lys Pro Asp Glu Leu His Lys Ser Ser Lys
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209 Phe Thr Gly Leu Met Glu Asn Met Lys Val Leu Tyr Asp Asp Asn His
                                     25
213 Val Ser Ala Ile Asn Val Lys Ser Ile Asp Gln Phe Leu Tyr Phe Asp
            35
                                40
217 Leu Ile Tyr Ser Ile Lys Asp Thr Lys Leu Gly Asn Tyr Asp Asn Val
221 Arg Val Glu Phe Lys Asn Lys Asp Leu Ala Asp Lys Tyr Lys Asp Lys
225 Tyr Val Asp Val Phe Gly Ala Asn Tyr Tyr Tyr Gln Cys Tyr Phe Ser
226
                                         90
```

Input Set : A:\sequence listing.txt
Output Set: N:\CRF4\09152005\I150947G.raw

229 Lys Lys Thr Asn Asp Ile Asn Ser His Glu Thr Asp Lys Arg Lys Thr 230 105 110 233 Cys Met Tyr Gly Gly Val Thr Glu His Asn Gly Asn Gln Leu Asp Lys 115 120 237 Tyr Arg Ser Ile Thr Val Arg Val Phe Glu Asp Gly Lys Asn Leu Leu 130 135 241 Ser Phe Asp Val Gln Thr Asn Lys Lys Val Thr Ala Gln Glu Leu 242 145 150 155 245 Asp Tyr Leu Thr Arg His Tyr Leu Val Lys Asn Lys Lys Leu Tyr Glu 170 249 Phe Asn Asn Ser Pro Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Glu Asn 250 180 185 253 Glu Asn Ser Phe Trp Tyr Asp Met Met Pro Ala Pro Gly Asp Lys Phe 200 257 Asp Gln Ser Lys Tyr Leu Met Met Tyr Asn Asp Asn Lys Met Val Asp 258 210 215 261 Ser Lys Asp Val Lys Ile Glu Val Tyr Leu Thr Thr Lys Lys 230 265 <210> SEQ ID NO: 13 266 <211> LENGTH: 10 267 <212> TYPE: PRT 268 <213> ORGANISM: Artificial 270 <220> FEATURE: 271 <223> OTHER INFORMATION: Consensus sequence 274 <220> FEATURE: 275 <221> NAME/KEY: UNSURE 276 <222> LOCATION: (3)..(6) 277 <223> OTHER INFORMATION: Any amino acid 279 <400> SEQUENCE: 13 W--> 281 Lys Lys Xaa Xaa Xaa Gln Glu Leu Asp 282 1 285 <210> SEQ ID NO: 14 286 <211> LENGTH: 12 287 <212> TYPE: PRT 288 <213> ORGANISM: Artificial 290 <220> FEATURE: 291 <223> OTHER INFORMATION: Consensus sequence 294 <220> FEATURE: 295 <221> NAME/KEY: UNSURE 296 <222> LOCATION: (1)..(2) 297 <223> OTHER INFORMATION: Any amino acid 299 <220> FEATURE: 300 <221> NAME/KEY: UNSURE 301 <222> LOCATION: (5)..(8) 302 <223> OTHER INFORMATION: Any amino acid 304 <400> SEQUENCE: 14 W--> 306 Xaa Xaa Lys Lys Xaa Xaa Xaa Xaa Gln Glu Leu Asp

310 <210> SEQ ID NO: 15

307 1

Input Set : A:\sequence listing.txt

Output Set: N:\CRF4\09152005\I150947G.raw

- 311 <211> LENGTH: 11 312 <212> TYPE: PRT 313 <213> ORGANISM: Artificial 315 <220> FEATURE: 316 <223> OTHER INFORMATION: Consensus sequence 319 <220> FEATURE: 320 <221> NAME/KEY: misc\_feature 321 <222> LOCATION: (1)..(1) 322 <223> OTHER INFORMATION: Can be either Tyr or Thr 324 <220> FEATURE: 325 <221> NAME/KEY: UNSURE 326 <222> LOCATION: (3)..(8) 327 <223> OTHER INFORMATION: Any amino acid 329 <220> FEATURE: 330 <221> NAME/KEY: UNSURE 331 <222> LOCATION: (10)..(10) 332 <223> OTHER INFORMATION: Any amino acid
- W--> **336** Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Asp 337 1 5 10

334 <400> SEQUENCE: 15

Input Set : A:\sequence listing.txt

Output Set: N:\CRF4\09152005\I150947G.raw

#### Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; Xaa Pos. 3,4,5,6// Seq#:14; Xaa Pos. 1,2,5,6/7,8/ Seq#:15; Xaa Pos. 1,3,4,5,6,7,8,10

### Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:13,14,15

#### VERIFICATION SUMMARY

DATE: 09/15/2005 PATENT APPLICATION: US/09/150,947G TIME: 11:40:47

Input Set : A:\sequence listing.txt

Output Set: N:\CRF4\09152005\I150947G.raw

L:281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0 L:306 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0 L:336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0